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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Petkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
- (ii) TITLE OF INVENTION: Retinoid Metabolizing Protein
- (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Torys LLP
 - (B) STREET: 3000 - 79 Wellington Street West
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5K 1N2
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 - (B) COMPUTER: COMPAQ, IBM PC compatible
 - (C) OPERATING SYSTEM: MS-DOS 5.1
 - (D) SOFTWARE: WORD PERFECT
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/668,482
 - (B) FILING DATE: September 25, 2000
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBERS: 08/667,546; 08/724,466; PCT/CA97/00440;
 - (B) FILING DATE: June 21, 1996; October 1, 1996; June 23, 1997;
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hunt, John C.
 - (B) REGISTRATION NUMBER: 36,424
 - (C) REFERENCE/DOCKET NUMBER: 32391-2005
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 865-8121
 - (B) TELEFAX: (416) 865-7380

(2) INFORMATION FOR SEQ ID NO:1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

TGCCAGTGGA CAATCTCCCT ACCAAATTCA CTAGTTATGT CCAGAAATTA GCCTAAACCG	60
GAGCCTTTGT ACATATGTTT TTATTTTAGA TGAAGTGTGA TGTATTGGAT ATTTTCTAAT	120
TTGTTTATAT AAAGCAGATG TGTATATAAG TCTATGCGAA GAAGCGAAAA CGAGGGCACT	180

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ACTTTCTCAT GGATCACTGT AATGCTACAG AGTGTCTGTG ATGTATATTT ATAATGTAGT 240
 TGTGTCATAT AGCTTTTGTA CTGTATGCAA CTTATTTAAC TCGCTCTTTA TCTCATGGGT 300
 TTTATTTAAT AAAACATGTT CTTACAAAAA AAAAAAA 337

(2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Met Gly Leu Tyr Thr Leu Met Val Thr Phe Leu Cys Thr Ile Val Leu
 1 5 10 15
 Pro Val Leu Leu Phe Leu Ala Ala Val Lys Leu Trp Glu Met Leu Met
 20 25 30
 Ile Arg Arg Val Asp Pro Asn Cys Arg Ser Pro Leu Pro Pro Gly Thr
 35 40 45
 Met Gly Leu Pro Phe Ile Gly Glu Thr Leu Gln Leu Ile Leu Gln Arg
 50 55 60
 Arg Lys Phe Leu Arg Met Lys Arg Gln Lys Tyr Gly Cys Ile Tyr Lys
 65 70 75 80
 Thr His Leu Phe Gly Asn Pro Thr Val Arg Val Met Gly Ala Asp Asn
 85 90 95
 Val Arg Gln Ile Leu Leu Gly Glu His Lys Leu Val Ser Val Gln Trp
 100 105 110
 Pro Ala Ser Val Arg Thr Ile Leu Gly Ser Asp Thr Leu Ser Asn Val
 115 120 125
 His Gly Val Gln His Lys Asn Lys Lys Lys Ala Ile Met Arg Ala Phe
 130 135 140
 Ser Arg Asp Ala Leu Glu His Tyr Ile Pro Val Ile Gln Gln Glu Val
 145 150 155 160
 Lys Ser Ala Ile Gln Glu Trp Leu Gln Lys Asp Ser Cys Val Leu Val
 165 170 175
 Tyr Pro Glu Met Lys Lys Leu Met Phe Arg Ile Ala Met Arg Ile Leu
 180 185 190
 Leu Gly Phe Glu Pro Glu Gln Ile Lys Thr Asp Glu Gln Glu Leu Val
 195 200 205

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Glu Ala Phe Glu Glu Met Ile Lys Asn Leu Phe Ser Leu Pro Ile Asp
 210 215 220
 Val Pro Phe Ser Gly Leu Tyr Arg Gly Leu Arg Ala Arg Asn Phe Ile
 225 230 235 240
 His Ser Lys Ile Glu Glu Asn Ile Arg Lys Lys Ile Gln Asp Asp Asp
 245 250 255
 Asn Glu Asn Glu Gln Lys Tyr Lys Asp Ala Leu Gln Leu Leu Ile Glu
 260 265 270
 Asn Ser Arg Arg Ser Asp Glu Pro Phe Ser Leu Gln Ala Met Lys Glu
 275 280 285
 Ala Ala Thr Glu Leu Leu Phe Gly Gly His Glu Thr Thr Ala Ser Thr
 290 295 300
 Ala Thr Ser Leu Val Met Phe Leu Gly Leu Asn Thr Glu Val Val Gln
 305 310 315 320
 Lys Val Arg Glu Glu Val Gln Glu Lys Val Glu Met Gly Met Tyr Thr
 325 330 335
 Pro Gly Lys Gly Leu Ser Met Glu Leu Leu Asp Gln Leu Lys Tyr Thr
 340 345 350
 Gly Cys Val Ile Lys Glu Thr Leu Arg Ile Asn Pro Pro Val Pro Gly
 355 360 365
 Gly Phe Arg Val Ala Leu Lys Thr Phe Glu Leu Asn Gly Tyr Gln Ile
 370 375 380
 Pro Lys Gly Trp Asn Val Ile Tyr Ser Ile Cys Asp Thr His Asp Val
 385 390 395 400
 Ala Asp Val Phe Pro Asn Lys Glu Glu Phe Gln Pro Glu Arg Phe Met
 405 410 415
 Ser Lys Gly Leu Glu Asp Gly Ser Arg Phe Asn Tyr Ile Pro Phe Gly
 420 425 430
 Gly Gly Ser Arg Met Cys Val Gly Lys Glu Phe Ala Lys Val Leu Leu
 435 440 445
 Lys Ile Phe Leu Val Glu Leu Thr Gln His Cys Asn Trp Ile Leu Ser
 450 455 460
 Asn Gly Pro Pro Thr Met Lys Thr Gly Pro Thr Ile Tyr Pro Val Asp
 465 470 475 480
 Asn Leu Pro Thr Lys Phe Thr Ser Tyr Val Arg Asn
 485 490

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(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1850 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

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TGTCGCCGTT GCTGTCGGTT GCTGTCGGAC GCTGTCTCCT CTCCAGAAGC TTGTTTTTCG      60
TTTTGGCGAT CAGTTGCGCG CTTCAAC ATG GGG CTG TAC ACC CTT ATG GTC ACC      114
          Met Gly Leu Tyr Thr Leu Met Val Thr
          1                      5

TTT CTC TGC ACC ATC GTG CTA CCC GTT TTA CTC TTT CTC GCC GCG GTG      162
Phe Leu Cys Thr Ile Val Leu Pro Val Leu Leu Phe Leu Ala Ala Val
10                      15                      20                      25

AAG TTG TGG GAG ATG TTA ATG ATC CGA CGA GTC GAT CCG AAC TGC AGA      210
Lys Leu Trp Glu Met Leu Met Ile Arg Arg Val Asp Pro Asn Cys Arg
          30                      35                      40

AGT CCT CTA CCG CCA GGT ACC ATG GGC TTG CCG TTC ATT GGA GAA ACG      258
Ser Pro Leu Pro Pro Gly Thr Met Gly Leu Pro Phe Ile Gly Glu Thr
          45                      50                      55

CTC CAG CTG ATC CTC CAG AGA AGG AAG TTT CTG CGC ATG AAA CGG CAG      306
Leu Gln Leu Ile Leu Gln Arg Arg Lys Phe Leu Arg Met Lys Arg Gln
60                      65                      70

AAA TAC GGG TGC ATC TAC AAG ACG CAC CTC TTC GGG AAC CCG ACT GTC      354
Lys Tyr Gly Cys Ile Tyr Lys Thr His Leu Phe Gly Asn Pro Thr Val
75                      80                      85

AGG GTG ATG GGA GCT GAT AAT GTG AGG CAG ATT CTG CTG GGC GAA CAC      402
Arg Val Met Gly Ala Asp Asn Val Arg Gln Ile Leu Leu Gly Glu His
90                      95                      100                      105

AAG CTG GTG TCT GTT CAG TGG CCA GCA TCA GTG AGA ACC ATC CTG GGC      450
Lys Leu Val Ser Val Gln Trp Pro Ala Ser Val Arg Thr Ile Leu Gly
110                      115                      120

TCT GAC ACC CTC TCC AAT GTC CAT GGA GTT CAA CAC AAA AAC AAG AAA      498
Ser Asp Thr Leu Ser Asn Val His Gly Val Gln His Lys Asn Lys Lys
125                      130                      135

AAG GCC ATT ATG AGG GCG TTC TCT CGA GAT GCT CTG GAG CAC TAC ATT      546
Lys Ala Ile Met Arg Ala Phe Ser Arg Asp Ala Leu Glu His Tyr Ile
140                      145                      150

CCC GTG ATC CAG CAG GAG GTG AAG AGC GCC ATA CAG GAA TGG CTG CAA      594
Pro Val Ile Gln Gln Glu Val Lys Ser Ala Ile Gln Glu Trp Leu Gln
155                      160                      165

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AAA GAC TCC TGC GTG CTG GTT TAT CCA GAA ATG AAG AAA CTC ATG TTT Lys Asp Ser Cys Val Leu Val Tyr Pro Glu Met Lys Lys Leu Met Phe 170 175 180 185	642
CGG ATA GCT ATG AGA ATC CTG CTT GGT TTT GAA CCA GAG CAA ATA AAG Arg Ile Ala Met Arg Ile Leu Leu Gly Phe Glu Pro Glu Gln Ile Lys 190 195 200	690
ACG GAC GAG CAA GAA CTG GTG GAA GCT TTT GAG GAA ATG ATC AAA AAC Thr Asp Glu Gln Glu Leu Val Glu Ala Phe Glu Glu Met Ile Lys Asn 205 210 215	738
TTG TTC TCC TTG CCA ATC GAC GTT CCT TTC AGT GGT CTG TAC AGG GGT Leu Phe Ser Leu Pro Ile Asp Val Pro Phe Ser Gly Leu Tyr Arg Gly 220 225 230	786
TTG AGG GCA CGC AAT TTC ATT CAC TCC AAA ATT GAG GAA AAC ATC AGG Leu Arg Ala Arg Asn Phe Ile His Ser Lys Ile Glu Glu Asn Ile Arg 235 240 245	834
AAG AAA ATT CAA GAT GAC GAC AAT GAA AAC GAA CAG AAA TAC AAA GAC Lys Lys Ile Gln Asp Asp Asp Asn Glu Asn Glu gln Lys Tyr Lys Asp 250 255 260 265	882
GCC CTT CAG CTG TTG ATC GAG AAC AGC AGA AGA AGT GAC GAA CCT TTT Ala Leu Gln Leu Leu Ile Glu Asn Ser Arg Arg Ser Asp Glu Pro Phe 270 275 280	930
AGT TTG CAG GCG ATG AAA GAA GCA GCT ACA GAG CTT CTA TTT GGA GGT Ser Leu Gln Ala Met Lys Glu Ala Ala Thr Glu Leu Leu Phe Gly Gly 285 290 295	978
CAT GAA ACC ACC GCC AGC ACT GCA ACC TCA CTT GTC ATG TTT CTG GGT His Glu Thr Thr Ala Ser Thr Ala Thr Ser Leu Val Met Phe Leu Gly 300 305 310	1026
CTG AAC ACA GAA GTG GTG CAG AAG GTC AGA GAG GAG GTT CAG GAG AAG Leu Asn Thr Glu Val Val Gln Lys Val Arg Glu Glu Val Gln Glu Lys 315 320 325	1074
GTT GAA ATG GGC ATG TAT ACA CCT GGA AAG GGC TTG AGT ATG GAG CTG Val Glu Met Gly Met Tyr Thr Pro Gly Lys Gly Leu Ser Met Glu Leu 330 335 340 345	1122
TTG GAC CAG CTG AAG TAC ACT GGA TGT GTG ATT AAA GAG ACT CTT AGA Leu Asp Gln Leu Lys Tyr Thr Gly Cys Val Ile Lys Glu Thr Leu Arg 350 355 360	1170
ATC AAC CCT CCT GTT CCC GGA GGA TTC AGA GTC GCA CTC AAA ACC TTT Ile Asn Pro Pro Val Pro Gly Gly Phe Arg Val Ala Leu Lys Thr Phe 365 370 375	1218
GAA TTG AAT GGT TAC CAA ATT CCT AAA GGA TGG AAC GTC ATT TAC AGC Glu Leu Asn Gly Tyr Gln Ile Pro Lys Gly Trp Asn Val Ile Tyr Ser 380 385 390	1266

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ATC TGT GAC ACG CAC GAT GTG GCC GAC GTC TTT CCA AAC AAA GAG GAG Ile Cys Asp Thr His Asp Val Ala Asp Val Phe Pro Asn Lys Glu Glu 395 400 405	1314
TTC CAG CCG GAG AGA TTC ATG AGC AAA GGT CTG GAG GAC GGG TCC AGG Phe Gln Pro Glu Arg Phe Met Ser Lys Gly Leu Glu Asp Gly Ser Arg 410 415 420 425	1362
TTT AAC TAC ATC CCC TTC GGA GGA GGA TCC AGG ATG TGT GTG GGC AAA Phe Asn Tyr Ile Pro Phe Gly Gly Gly Ser Arg Met Cys Val Gly Lys 430 435 440	1410
GAG TTC GCC AAA GTG TTA CTC AAG ATC TTT TTA GTT GAG TTA ACG CAG Glu Phe Ala Lys Val Leu Leu Lys Ile Phe Leu Val Glu Leu Thr Gln 445 450 455	1458
CAT TGC AAT TGG ATT CTC TCA AAC GGA CCC CCG ACA ATG AAA ACA GGC His Cys Asn Trp Ile Leu Ser Asn Gly Pro Pro Thr Met Lys Thr Gly 460 465 470	1506
CCG ACT ATT TAC CCA GTG GAC AAT CTC CCT ACC AAA TTC ACT AGT TAT Pro Thr Ile Tyr Pro Val Asp Asn Leu Pro Thr Lys Phe Thr Ser Tyr 475 480 485	1554
GTC AGA AAT TAGCCTAACC GGAGCTTTGT ACATATGTTT TTATTTTAGA Val Arg Asn 490	1603
TGAACTGTGA TGTATTGGAT ATTTTCTATT TTGTTTATAT AAAGCAGATG TGTATATAAG	1663
TCTATGCGAG GAAGCGAAAA CGAGGGCACT ACTTTCTCAT GGATCACTGT AATGCTACAG	1723
AGTGTCTGTG ATGTATATTT ATAATGTAGT TGTGTTATAT AGCTTTTGTA CTGTATGCAA	1783
CTTATTTAAC TCGCTCTTTA TCTCATGGGT TTTATTTAAT AAAACATGTT CTTACAAAAA	1843
AAAAAAA	1850

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Met Gly Leu Pro Ala Leu Leu Ala Ser Ala Leu Cys Thr Phe Val Leu 1 5 10 15
Pro Leu Leu Leu Phe Leu Ala Ala Ile Lys Leu Trp Asp Leu Tyr Cys 20 25 30
Val Ser Gly Arg Asp Arg Ser Cys Ala Leu Pro Leu Pro Pro Gly Thr 35 40 45

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Met Gly Phe Pro Phe Phe Gly Glu Thr Leu Gln Met Val Leu Gln Arg
 50 55 60

Arg Lys Phe Leu Gln Met Lys Arg Arg Lys Tyr Gly Phe Ile Tyr Lys
 65 70 75 80

Thr His Leu Phe Gly Arg Pro Thr Val Arg Val Met Gly Ala Asp Asn
 85 90 95

Val Arg Arg Ile Leu Leu Gly Asp Asp Arg Leu Val Ser Val His Trp
 100 105 110

Pro Ala Ser Val Arg Thr Ile Leu Gly Ser Gly Cys Leu Ser Asn Leu
 115 120 125

His Asp Ser Ser His Lys Gln Arg Lys Lys Val Ile Met Arg Ala Phe
 130 135 140

Ser Arg Glu Ala Leu Glu Cys Tyr Val Pro Val Ile Thr Glu Glu Val
 145 150 155 160

Gly Ser Ser Leu Glu Gln Trp Leu Ser Cys Gly Glu Arg Gly Leu Leu
 165 170 175

Val Tyr Pro Glu Val Lys Arg Leu Met Phe Arg Ile Ala Met Arg Ile
 180 185 190

Leu Leu Gly Cys Glu Pro Gln Leu Ala Gly Asp Gly Asp Ser Glu Gln
 195 200 205

Gln Leu Val Glu Ala Phe Glu Glu Met Thr Arg Asn Leu Phe Ser Leu
 210 215 220

Pro Ile Asp Val Pro Phe Ser Gly Leu Tyr Arg Gly Met Lys Ala Arg
 225 230 235 240

Asn Leu Ile His Ala Arg Ile Glu Gln Asn Ile Arg Ala Lys Ile Cys
 245 250 255

Gly Leu Arg Ala Ser Glu Ala Gly Gln Gly Cys Lys Asp Ala Leu Gln
 260 265 270

Leu Leu Ile Glu His Ser Trp Glu Arg Gly Glu Arg Leu Asp Met Gln
 275 280 285

Ala Leu Lys Gln Ser Ser Thr Glu Leu Leu Phe Gly Gly His Glu Thr
 290 295 300

Thr Ala Ser Ala Ala Thr Ser Leu Ile Thr Tyr Leu Gly Leu Tyr Pro
 305 310 315 320

His Val Leu Gln Lys Val Arg Glu Glu Leu Lys Ser Lys Gly Leu Leu
 325 330 335

Cys Lys Ser Asn Gln Asp Asn Lys Leu Asp Met Glu Ile Leu Glu Gln
 340 345 350

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Leu Lys Tyr Ile Gly Cys Val Ile Lys Glu Thr Leu Arg Leu Asn Pro
 355 360 365
 Pro Val Pro Gly Gly Phe Arg Val Ala Leu Lys Thr Phe Glu Leu Asn
 370 375 380
 Gly Tyr Gln Ile Pro Lys Gly Trp Asn Val Ile Tyr Ser Ile Cys Asp
 385 390 395 400
 Thr His Asp Val Ala Glu Ile Phe Thr Asn Lys Glu Glu Phe Asn Pro
 405 410 415
 Asp Arg Phe Ser Ala Pro His Pro Glu Asp Ala Ser Arg Phe Ser Phe
 420 425 430
 Ile Pro Phe Gly Gly Gly Leu Arg Ser Cys Val Gly Lys Glu Phe Ala
 435 440 445
 Lys Ile Leu Leu Lys Ile Phe Thr Val Glu Leu Ala Arg His Cys Asp
 450 455 460
 Trp Gln Leu Leu Asn Gly Pro Pro Thr Met Lys Thr Ser Pro Thr Val
 465 470 475 480
 Tyr Pro Val Asp Asn Leu Pro Ala Arg Phe Thr His Phe His Gly Glu
 485 490 495
 Ile

(2) INFORMATION FOR SEQ ID NO:5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

ATG GGG CTC CCG GCG CTG CTG GCC AGT GCG CTC TGC ACC TTC GTG CTG	48
Met Gly Leu Pro Ala Leu Leu Ala Ser Ala Leu Cys Thr Phe Val Leu	
1 5 10 15	
CCG CTG CTG CTC TTC CTG GCT GCG ATC AAG CTC TGG GAC CTG TAC TGC	96
Pro Leu Leu Leu Phe Leu Ala Ala Ile Lys Leu Trp Asp Leu Tyr Cys	
20 25 30	
GTG AGC GGC CGC GAC CGC AGT TGT GCC CTC CCA TTG CCC CCC GGG ACT	144
Val Ser Gly Arg Asp Arg Ser Cys Ala Leu Pro Leu Pro Pro Gly Thr	
35 40 45	
ATG GGC TTC CCC TTC TTT GGG GAA ACC TTG CAG ATG GTA CTG CAG CGG	192
Met Gly Phe Pro Phe Phe Gly Glu Thr Leu Gln Met Val Leu Gln Arg	
50 55 60	

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AGG AAG TTC CTG CAG ATG AAG CGC AGG AAA TAC GGC TTC ATC TAC AAG	240
Arg Lys Phe Leu Gln Met Lys Arg Arg Lys Tyr Gly Phe Ile Tyr Lys	
65 70 75 80	
ACG CAT CTG TTC GGG CGG CCC ACC GTA CGG GTG ATG GGC GCG GAC AAT	288
Thr His Leu Phe Gly Arg Pro Thr Val Arg Val Met Gly Ala Asp Asn	
85 90 95	
GTG CGG CGC ATC TTG CTC GGA GAC GAC CGG CTG GTG TCG GTC CAC TGG	336
Val Arg Arg Ile Leu Leu Gly Asp Asp Arg Leu Val Ser Val His Trp	
100 105 110	
CCA GCG TCG GTG CGC ACC ATT CTG GGA TCT GGC TGC CTC TCT AAC CTG	384
Pro Ala Ser Val Arg Thr Ile Leu Gly Ser Gly Cys Leu Ser Asn Leu	
115 120 125	
CAC GAC TCC TCG CAC AAG CAG CGC AAG AAG GTG ATT ATG CGG GCC TTC	432
His Asp Ser Ser His Lys Gln Arg Lys Lys Val Ile Met Arg Ala Phe	
130 135 140	
AGC CGC GAG GCA CTC GAA TGC TAC GTG CCG GTG ATC ACC GAG GAA GTG	480
Ser Arg Glu Ala Leu Glu Cys Tyr Val Pro Val Ile Thr Glu Glu Val	
145 150 155 160	
GGC AGC AGC CTG GAG CAG TGG CTG AGC TGC GGC GAG CGC GGC CTC CTG	528
Gly Ser Ser Leu Glu Gln Trp Leu Ser Cys Gly Glu Arg Gly Leu Leu	
165 170 175	
GTC TAC CCC GAG GTG AAG CGC CTC ATG TTC CGA ATC GCC ATG CGC ATC	576
Val Tyr Pro Glu Val Lys Arg Leu Met Phe Arg Ile Ala Met Arg Ile	
180 185 190	
CTA CTG GGC TGC GAA CCC CAA CTG GCG GGC GAC GGG GAC TCC GAG CAG	624
Leu Leu Gly Cys Glu Pro Gln Leu Ala Gly Asp Gly Asp Ser Glu Gln	
195 200 205	
CAG CTT GTG GAG GCC TTC GAG GAA ATG ACC CGC AAT CTC TTC TCG CTG	672
Gln Leu Val Glu Ala Phe Glu Glu Met Thr Arg Asn Leu Phe Ser Leu	
210 215 220	
CCC ATC GAC GTG CCC TTC AGC GGG CTG TAC CGG GGC ATG AAG GCG CGG	720
Pro Ile Asp Val Pro Phe Ser Gly Leu Tyr Arg Gly Met Lys Ala Arg	
225 230 235 240	
AAC CTC ATT CAC GCG CGC ATC GAG CAG AAC ATT CGC GCC AAG ATC TGC	768
Asn Leu Ile His Ala Arg Ile Glu Gln Asn Ile Arg Ala Lys Ile Cys	
245 250 255	
GGG CTG CGG GCA TCC GAG GCG GGC CAG GGC TGC AAA GAC GCG CTG CAG	816
Gly Leu Arg Ala Ser Glu Ala Gly Gln Gly Cys Lys Asp Ala Leu Gln	
260 265 270	
CTG TTG ATC GAG CAC TCG TGG GAG AGG GGA GAG CGG CTG GAC ATG CAG	864
Leu Leu Ile Glu His Ser Trp Glu Arg Gly Glu Arg Leu Asp Met Gln	
275 280 285	

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GCA CTA AAG CAA TCT TCA ACC GAA CTC CTC TTT GGA GGA CAC GAA ACC Ala Leu Lys Gln Ser Ser Thr Glu Leu Leu Phe Gly Gly His Glu Thr 290 295 300	912
ACG GCC AGT GCA GCC ACA TCT CTG ATC ACT TAC CTG GGG CTC TAC CCA Thr Ala Ser Ala Ala Thr Ser Leu Ile Thr Tyr Leu Gly Leu Tyr Pro 305 310 315 320	960
CAT GTT CTC CAG AAA GTG CGA GAA GAG CTG AAG AGT AAG GGT TTA CTT His Val Leu Gln Lys Val Arg Glu Glu Leu Lys Ser Lys Gly Leu Leu 325 330 335	1008
TGC AAG AGC AAT CAA GAC AAC AAG TTG GAC ATG GAA ATT TTG GAA CAA Cys Lys Ser Asn Gln Asp Asn Lys Leu Asp Met Glu Ile Leu Glu Gln 340 345 350	1056
CTT AAA TAC ATC GGG TGT GTT ATT AAG GAG ACC CTT CGA CTG AAT CCC Leu Lys Tyr Ile Gly Cys Val Ile Lys Glu Thr Leu Arg Leu Asn Pro 355 360 365	1104
CCA GTT CCA GGA GGG TTT CGG GTT GCT CTG AAG ACT TTT GAA TTA AAT Pro Val Pro Gly Gly Phe Arg Val Ala Leu Lys Thr Phe Glu Leu Asn 370 375 380	1152
GGA TAC CAG ATT CCC AAG GGC TGG AAT GTT ATC TAC AGT ATC TGT GAT Gly Tyr Gln Ile Pro Lys Gly Trp Asn Val Ile Tyr Ser Ile Cys Asp 385 390 395 400	1200
ACT CAT GAT GTG GCA GAG ATC TTC ACC AAC AAG GAA GAA TTT AAT CCT Thr His Asp Val Ala Glu Ile Phe Thr Asn Lys Glu Glu Phe Asn Pro 405 410 415	1248
GAC CGA TTC AGT GCT CCT CAC CCA GAG GAT GCA TCC AGG TTC AGC TTC Asp Arg Phe Ser Ala Pro His Pro Glu Asp Ala Ser Arg Phe Ser Phe 420 425 430	1296
ATT CCA TTT GGA GGA GGC CTT AGG AGC TGT GTA GGC AAA GAA TTT GCA Ile Pro Phe Gly Gly Gly Leu Arg Ser Cys Val Gly Lys Glu Phe Ala 435 440 445	1344
AAA ATT CTT CTC AAA ATA TTT ACA GTG GAG CTG GCC AGG CAT TGT GAC Lys Ile Leu Leu Lys Ile Phe Thr Val Glu Leu Ala Arg His Cys Asp 450 455 460	1392
TGG CAG CTT CTA AAT GGA CCT CCT ACA ATG AAA ACC AGT CCC ACC GTG Trp Gln Leu Leu Asn Gly Pro Pro Thr Met Lys Thr Ser Pro Thr Val 465 470 475 480	1440
TAT CCT GTG GAC AAT CTC CCT GCA AGA TTC ACC CAT TTC CAT GGG GAA Tyr Pro Val Asp Asn Leu Pro Ala Arg Phe Thr His Phe His Gly Glu 485 490 495	1488
ATC TGA Ile	1494

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(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Pro Phe Gly Gly Gly Pro Arg Leu Cys Pro Gly Tyr Glu Leu Ala Arg
1 5 10 15

Val Ala Leu Ser
20

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Pro Phe Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
1 5 10 15

Ser Glu Met Lys
20

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

Pro Phe Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
1 5 10 15

Asn Glu Leu Lys
20

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala Ile
 1 5 10 15
 Met Asn Met Lys
 20

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Pro Phe Ser Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met
 1 5 10 15
 Asn Glu Leu Lys
 20

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

GAAGTCCTCT TTGGAGGACA CGAAACCACG GCCAGTGCAG CCACATCTCT GATCACTTAC 60
 CTGGGGCTCT ACCCACATGT TCTCCAGAAA GTGCGAGAAG AGCTGAAGAG TAAGGGTTTA 120
 CTTTGCAAGA GCAATCAAGA CAACAAGTTG GACATGGAAA TTTTGGAACA ACTTAAATAC 180
 ATCGGGTGTG TTATTAAGGA GACCCCTTCGA CTGAATCCCC CAGTTCCAGG AGGGTTTCGG 240
 GTTGCTCTGA AGACTTTTGA ATTAAATGGA TACCAGATTC CCAAGGGCTG GAATGTTATC 300
 TACAGTATCT GTGATACTCA TGATGTGGCA GAGATCTTCA CCAACAAGGA A 351

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

TTTTTTTTTT TTGG

14

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- (2) INFORMATION FOR SEQ ID NO:13
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

TTTTTTTTTT TTGA

14

- (2) INFORMATION FOR SEQ ID NO:14
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

TTTTTTTTTT TTGT

14

- (2) INFORMATION FOR SEQ ID NO:15
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

TTTTTTTTTT TTGC

14

- (2) INFORMATION FOR SEQ ID NO:16
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

TTTTTTTTTT TTAG

14

- (2) INFORMATION FOR SEQ ID NO:17
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

TTTTTTTTTT TTAA

14

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

TTTTTTTTTT TTAT

14

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TTTTTTTTTT TTAC

14

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

TTTTTTTTTT TTCG

14

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

TTTTTTTTTT TTCA

14

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(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

TTTTTTTTTT TTCT

14

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

TTTTTTTTTT TTCC

14

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

AAGCGACCGA

10

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

TGTTGCCAG

10

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

TGCCAGTGGA

10

(2) INFORMATION FOR SEQ ID NO:27

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

GGCTGCAAAC

10

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

CCTAGCGTTG

10

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

GTAGCGGCCG CTGCCAGTGG A

21

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

GTAGCGGCCG CT

12

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(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

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GCACGAGGGA GGCTGAAGCG TGCC ATG GGG CTC CCG GCG CTG CTG GCC AGT      51
                Met Gly Leu Pro Ala Leu Leu Ala Ser
                1                    5

GCG CTC TGC ACC TTC GTG CTG CCG CTG CTG CTC TTC CTG GCG GCG CTC      99
Ala Leu Cys Thr Phe Val Leu Pro Leu Leu Leu Phe Leu Ala Ala Leu
10                15                20                25

AAG CTC TGG GAC CTG TAC TGT GTG AGC AGC CGC GAT CGC AGC TGC GCC      147
Lys Leu Trp Asp Leu Tyr Cys Val Ser Ser Arg Asp Arg Ser Cys Ala
                30                35                40

CTC CCC TTG CCC CCC GGT ACC ATG GGC TTC CCA TTC TTT GGG GAA ACA      195
Leu Pro Leu Pro Pro Gly Thr Met Gly Phe Pro Phe Phe Gly Glu Thr
                45                50                55

TTG CAG ATG GTG CTT CAG CGG AGG AAG TTT CTG CAG ATG AAG CGC AGG      243
Leu Gln Met Val Leu Gln Arg Arg Lys Phe Leu Gln Met Lys Arg Arg
                60                65                70

AAA TAC GGC TTC ATC TAC AAG ACG CAT CTG TTT GGG CGG CCC ACG GTG      291
Lys Tyr Gly Phe Ile Tyr Lys Thr His Leu Phe Gly Arg Pro Thr Val
                75                80                85

CGG GTG ATG GGC GCG GAT AAT GTG CGG CGC ATC TTG CTG GGA GAG CAC      339
Arg Val Met Gly Ala Asp Asn Val Arg Arg Ile Leu Leu Gly Glu His
90                95                100                105

CGG TTG GTG TCG GTG CAC TGG CCC GCG TCG GTG CGC ACC ATC CTG GGC      387
Arg Leu Val Ser Val His Trp Pro Ala Ser Val Arg Thr Ile Leu Gly
                110                115                120

GCT GGC TGC CTC TCC AAC CTG CAC GAT TCC TCG CAC AAG CAG CGA AAG      435
Ala Gly Cys Leu Ser Asn Leu His Asp Ser Ser His Lys Gln Arg Lys
                125                130                135

AAG GTG ATT ATG CAG GCC TTC AGC CGC GAG GCA CTC CAG TGC TAC GTG      483
Lys Val Ile Met Gln Ala Phe Ser Arg Glu Ala Leu Gln Cys Tyr Val
                140                145                150

CTC GTG ATC GCT GAG GAA GTC AGC AGT TGT CTG GAG CAG TGG CTA AGC      531
Leu Val Ile Ala Glu Glu Val Ser Ser Cys Leu Glu Gln Trp Leu Ser
                155                160                165

TGC GGC GAG CGC GGC CTC CTG GTC TAC CCC GAG GTG AAG CGC CTC ATG      579
Cys Gly Glu Arg Gly Leu Leu Val Tyr Pro Glu Val Lys Arg Leu Met
170                175                180                185

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TTC CGC ATC GCC ATG CGC ATC CTG CTG GGC TGC GAG CCG GGT CCA GCG	627
Phe Arg Ile Ala Met Arg Ile Leu Leu Gly Cys Glu Pro Gly Pro Ala	
190 195 200	
GGC GGC GGG GAG GAC GAG CAA CAG CTC GTG GAG GCT TTC GAG GAG ATG	675
Gly Gly Gly Glu Asp Glu Gln Gln Leu Val Glu Ala Phe Glu Glu Met	
205 210 215	
ACC CGC AAT CTC TTC TCT CTT CCC ATT GAC GTG CCC TTT AGC GGC CTG	723
Thr Arg Asn Leu Phe Ser Leu Pro Ile Asp Val Pro Phe Ser Gly Leu	
220 225 230	
TAC CGG GGC GTG AAG GCG CGG AAC CTT ATA CAC GCG CGC ATC GAG GAG	771
Tyr Arg Gly Val Lys Ala Arg Asn Leu Ile His Ala Arg Ile Glu Glu	
235 240 245	
AAC ATT CGC GCC AAG ATC CGC CGG CTT CAG GCT ACA GAG CCG GAT GGG	819
Asn Ile Arg Ala Lys Ile Arg Arg Leu Gln Ala Thr Glu Pro Asp Gly	
250 255 265	
GGT TGC AAG GAC GCG CTG CAG CTC CTG ATT GAG CAC TCG TGG GAG AGG	867
Gly Cys Lys Asp Ala Leu Gln Leu Leu Ile Glu His Ser Trp Glu Arg	
270 275 280	
GGA GAG AGG CTG GAT ATG CAG GCA CTA AAA CAA TCG TCA ACA GAG CTC	915
Gly Glu Arg Leu Asp Met Gln Ala Leu Lys Gln Ser Ser Thr Glu Leu	
285 290 295	
CTC TTT GGT GGT CAT GAA ACT ACA GCC AGT GCT GCG ACA TCA CTG ATC	963
Leu Phe Gly Gly His Glu Thr Thr Ala Ser Ala Ala Thr Ser Leu Ile	
300 305 310	
ACT TAC CTA GGA CTC TAC CCA CAT GTC CTC CAG AAA GTT CGA GAA GAG	1011
Thr Tyr Leu Gly Leu Tyr Pro His Val Leu Gln Lys Val Arg Glu Glu	
315 320 325	
ATA AAG AGC AAG GGC TTA CTT TGC AAG AGC AAT CAA GAC AAC AAG TTA	1059
Ile Lys Ser Lys Gly Leu Leu Cys Lys Ser Asn Gln Asp Asn Lys Leu	
330 335 340 345	
GAC ATG GAA ACT TTG GAA CAG CTT AAA TAC ATT GGG TGT GTC ATT AAG	1107
Asp Met Glu Thr Leu Glu Gln Leu Lys Tyr Ile Gly Cys Val Ile Lys	
350 355 360	
GAG ACC CTG CGA TTG AAT CCT CCG GTT CCA GGA GGG TTT CGG GTT GCT	1155
Glu Thr Leu Arg Leu Asn Pro Pro Val Pro Gly Gly Phe Arg Val Ala	
365 370 375	
CTG AAG ACT TTT GAG CTG AAT GGA TAC CAG ATC CCC AAG GGC TGG AAT	1203
Leu Lys Thr Phe Glu Leu Asn Gly Tyr Gln Ile Pro Lys Gly Trp Asn	
380 385 390	
GTT ATT TAC AGT ATC TGT GAC ACC CAC GAT GTG GCA GAT ATC TTC ACT	1251
Val Ile Tyr Ser Ile Cys Asp Thr His Asp Val Ala Asp Ile Phe Thr	
395 400 405	

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AAC AAG GAG GAA TTT AAT CCC GAC CGC TTT ATA GTG CCT CAT CCA GAG	1299
Asn Lys Glu Glu Phe Asn Pro Asp Arg Phe Ile Val Pro His Pro Glu	
410 415 420 425	
GAT GCT TCC CGG TTC AGC TTC ATT CCA TTT GGA GGA GGC CTT CGG AGC	1347
Asp Ala Ser Arg Phe Ser Phe Ile Pro Phe Gly Gly Gly Leu Arg Ser	
430 435 440	
TGT GTA GGC AAA GAG TTT GCA AAA ATT CTT CTT AAG ATA TTT ACA GTG	1395
Cys Val Gly Lys Glu Phe Ala Lys Ile Leu Leu Lys Ile Phe Thr Val	
445 450 455	
GAG CTG GCT AGG CAC TGT GAT TGG CAG CTT CTA AAT GGA CCT CCT ACA	1443
Glu Leu Ala Arg His Cys Asp Trp Gln Leu Leu Asn Gly Pro Pro Thr	
460 465 470	
ATG AAG ACA AGC CCC ACT GTG TAC CCT GTG GAC AAT CTC CCT GCA AGA	1491
Met Lys Thr Ser Pro Thr Val Tyr Pro Val Asp Asn Leu Pro Ala Arg	
475 480 485	
TTC ACC TAC TTC CAG GGA GAT ATC TGATAGCTAT TTCAATTCTT	1535
Phe Thr Tyr Phe Gln Gly Asp Ile	
490 495	
GGACTTATTT GAAGTGTATA TTGGTTTTTTT TTAAAAATAG TGTCATGTTG ACTTTATTTA	1595
ATTTCTAAAT GTATAGTATG ATATTTATGT GTCTCTACTA CAGTCCCGTG GTCTTTAAAT	1655
ATTAAATATA TGAATTTGTA TGATTTCCCA ATAAAGTAAA ATTAAAAAGT GAAAAAATAA	1715
AAAAAATAA	1725

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

Met Gly Leu Pro Ala Leu Leu Ala Ser Ala Leu Cys Thr Phe Val Leu	
1 5 10 15	
Pro Leu Leu Leu Phe Leu Ala Ala Leu Lys Leu Trp Asp Leu Tyr Cys	
20 25 30	
Val Ser Ser Arg Asp Arg Ser Cys Ala Leu Pro Leu Pro Pro Gly Thr	
35 40 45	
Met Gly Phe Pro Phe Phe Gly Glu Thr Leu Gln Met Val Leu Gln Arg	
50 55 60	
Arg Lys Phe Leu Gln Met Lys Arg Arg Lys Tyr Gly Phe Ile Tyr Lys	
65 70 75 80	

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Thr His Leu Phe Gly Arg Pro Thr Val Arg Val Met Gly Ala Asp Asn
 85 90 95
 Val Arg Arg Ile Leu Leu Gly Glu His Arg Leu Val Ser Val His Trp
 100 105 110
 Pro Ala Ser Val Arg Thr Ile Leu Gly Ala Gly Cys Leu Ser Asn Leu
 115 120 125
 His Asp Ser Ser His Lys Gln Arg Lys Lys Val Ile Met Gln Ala Phe
 130 135 140
 Ser Arg Glu Ala Leu Gln Cys Tyr Val Leu Val Ile Ala Glu Glu Val
 145 150 155 160
 Ser Ser Cys Leu Glu Gln Trp Leu Ser Cys Gly Glu Arg Gly Leu Leu
 165 170 175
 Val Tyr Pro Glu Val Lys Arg Leu Met Phe Arg Ile Ala Met Arg Ile
 180 185 190
 Leu Leu Gly Cys Glu Pro Gly Pro Ala Gly Gly Gly Glu Asp Glu Gln
 195 200 205
 Gln Leu Val Glu Ala Phe Glu Glu Met Thr Arg Asn Leu Phe Ser Leu
 210 215 220
 Pro Ile Asp Val Pro Phe Ser Gly Leu Tyr Arg Gly Val Lys Ala Arg
 225 230 235 240
 Asn Leu Ile His Ala Arg Ile Glu Glu Asn Ile Arg Ala Lys Ile Arg
 245 250 255
 Arg Leu Gln Ala Thr Glu Pro Asp Gly Gly Cys Lys Asp Ala Leu Gln
 260 265 270
 Leu Leu Ile Glu His Ser Trp Glu Arg Gly Glu Arg Leu Asp Met Gln
 275 280 285
 Ala Leu Lys Gln Ser Ser Thr Glu Leu Leu Phe Gly Gly His Glu Thr
 290 295 300
 Thr Ala Ser Ala Ala Thr Ser Leu Ile Thr Tyr Leu Gly Leu Tyr Pro
 305 310 315 320
 His Val Leu Gln Lys Val Arg Glu Glu Ile Lys Ser Lys Gly Leu Leu
 325 330 335
 Cys Lys Ser Asn Gln Asp Asn Lys Leu Asp Met Glu Thr Leu Glu Gln
 340 345 350
 Leu Lys Tyr Ile Gly Cys Val Ile Lys Glu Thr Leu Arg Leu Asn Pro
 355 360 365
 Pro Val Pro Gly Gly Phe Arg Val Ala Leu Lys Thr Phe Glu Leu Asn
 370 375 380

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Gly Tyr Gln Ile Pro Lys Gly Trp Asn Val Ile Tyr Ser Ile Cys Asp
 385 390 395 400
 Thr His Asp Val Ala Asp Ile Phe Thr Asn Lys Glu Glu Phe Asn Pro
 405 410 415
 Asp Arg Phe Ile Val Pro His Pro Glu Asp Ala Ser Arg Phe Ser Phe
 420 425 430
 Ile Pro Phe Gly Gly Gly Leu Arg Ser Cys Val Gly Lys Glu Phe Ala
 435 440 445
 Lys Ile Leu Leu Lys Ile Phe Thr Val Glu Leu Ala Arg His Cys Asp
 450 455 460
 Trp Gln Leu Leu Asn Gly Pro Pro Thr Met Lys Thr Ser Pro Thr Val
 465 470 475 480
 Tyr Pro Val Asp Asn Leu Pro Ala Arg Phe Thr Tyr Phe Gln Gly Asp
 485 490 495
 Ile

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

CGCACCCAG GAGGCGCGCT CGGAGGGAAG CCGCCACCGC CGCCGCCTCT GCCTCGGCGC 60
 GGAACAAACG GTTAAAGATT TTGGGCCASC GCCTCCGCGG GGGGAGGAGC CAGGGGCCCC 120
 AATCCCGCAA TTAAAGATGA ACTTTGGGTG AACTAATTGT CTGACCAAGG TAACGTGGGC 180
 AGCAACCTGG GCCGCCTATA AAGCGGCAGC GCCGTGGGGT TTGAAGCGCT GGCGGCGGCG 240
 GCAGGTGGCG CGGGAGGTCG CGGCGCGCCA TGG 273

(2) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

CGCACCCCA GGAGGCGCGC TCAGAGGGA GCGCCAGTG CGCCGCCTCT GCCTCGGCGC 60
 GGAACAAACG GTTAAAGATT TTTTGGGCA GCGCCTCGAG GGGGAGGAG CCAGGGGCCC 120

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GATCCGCAAT TAAAGATGAA CTTTGGGTGA ACTAATTTGT CTGACCAAGG TAACGTGGGC 180
AGTAACCTGG GCGGCCTTAT AAAGAGGGCG CGCGGCGGGG TTCGGAGCTA GGGAGGCGGC 240
GGCAGGTGGC GCGGGAGGCT GAAGCGTGCC ATGG 274

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

TCGGGGGAAT TAACACCTTT TCAAAGTGAA ATCTCAGGAT TGTCTGCCTT CTACAGGAGG 60
TGGTATTAAA ATGCGCCTAT AACAAATGGT TGAGAGTTTG GAGCCGCTTC TGCCCTGTGG 120
GCGGGGCGAG ATGACACCAC AATTAAAGAT GAACTTTGGG TGAACATAATT TATCTGAGGA 180
AGTTAACAGG AGGAGACCTG CGCGCAATGG ATATATAAGG GCGCGCAGGC GAGGACGCCC 240
TCASTTTGTG CGTAAAGACG CGTCTCCTCT CCAGAAGCTT GTTTTTCGTT TTGGCGATCA 300
GTTGCGCGCT TCAACATGG 319

(2) INFORMATION FOR SEQ ID NO:36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GATCCCAGAT CTGCCTATTG CGCCCGATGC CCCGAGGCTC TCTCTTGGAC TCTGGCCCTG 60
AGTTCTTCTG CGCGATCCTT CGGAGACGTC TGGAGGCCTG CTTTATGCAT CTCTCTTGGA 120
CCTCAGTTTC CCCACACGTG GGAGGAGGCA GCTGGACGAT TCCTGAAAGG ACTTTCCTT 180
GCTTCCTCAT CACGTGGAAG AGAGCCCACC CGGCACCTGG AAATGGAAAG CCAGTGAAGG 240
CTGCTTTGGG CCGGGGCAKC GGTGGGACC GGGCGGGAGG GATTCCAAAG AGACCGCCGG 300
GAAGGCTAGA GCTTGGAATT CCGGCTCCTC GGAGTCCTGG CCCTCCCCCA CCGCCGCCTC 360
GGAGCTCAGC ACACCTTGGA TGGGGGAGGC GGGCAGCTCC TAGCCCCGCA CCCCAGGAGG 420
CGCGCTCGGA GGAAGCCGC CACCGCCGCC GCCTCTGCCT CGGCGCGGAA CAAACGGTTA 480
AAGATTTTGG GCCASCGCCT CCGCGGGGGG AGGAGCCAGG GGCCCCAATC CCGCAATTAA 540
AGATGAACTT TGGGTGAACT AATTGTCTGA CCAAGGTAAC GTGGGCAGCA ACCTGGGCCG 600

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CCTATAAAGC GGCAGCGCCG TGGGGTTTGA AGCGCTGGCG GCGGCGGCAG GTGGCGCGGG	660
AGGTGCGGGC GCGCCATGGG GCTCCCGGCG CTGCTGGCCA GTGCGCTCTG CACCTTCGTG	720
CTGCCGCTGC TGCTCTTCCT GGCTGCGATC AAGCTCTGGG ACCTGTACTG CGTGAGCGGC	780
CGCGACCGCA GTTGTGCCCT CCCATTGCCC CCCGGGACTA TSGGSTTCCC CTTCTTTGGG	840
GAAACCTTGC AGATGNTACT NCAGGTAAGG GAGGGTGGGG CGGGACAGGC TGCTTCCCCG	900
GAGCCCGGCG CGGCTCTGGG CTTCTGCTGA AGTCGGGGTA GCGGCCCCCG GGAGGCATGC	960
TATTGCGGCT AGGAGCAGGG CTGGCGGGAG CGCGGCGCTC CCCGGMKYM C SCTCAWGCSC	1020
RCWWKTMWCC TCCGCCTYMC TCCCAMAGCG GARSAARWKC YKGMRGATGA AGCGCAGGAA	1080
ATACGGCTTC ATCTACAAGA CGCATCTGTT CGGGCGGCCC ACCGTACGGG TGATGGGCGC	1140
GGACAATGTG CGGCGCATCT TGCTCGGAGA GCACCGGCTG GTGTCCGTCC ACTGGCCAGC	1200
GTCCGTGCGC ACCATTCTGG GATCTGGCTG CCTCTCTAAC CTGCACGACT CCTCGCACAA	1260
GCAGCGCAAG AAGGTGGGGG CAGGAGGCGA CGGCTGGACA GGGAGGGGGA CCCCATTTAT	1320
GAGCGGAATT CCGGCTGATG GATGCTAGGC GCGGGCTAGC AGCTTGAGGT GGGCTAGGAC	1380
CCTCTGCCAG CTCCAGGTTA GCTTTCCCAG CTCGGAGAGT GCCATGTGTC TGGCAGGACT	1440
GGGGGTGTCT GGAAGGGGAC GGCGGTAGAC GAGAGGGGCG GATGGAGGCT TTTAACGCTG	1500
TCCCCTCCTC GGGACTCAGG TGATTATGCG GGCCTTCAGC CGCGAGGCAC TCGAATGCTA	1560
CGTGCCGGTG ATCACCAGAG AAGTGGGCAG CAGCCTGGAG CAGTGGCTGA GCTGCGGCGA	1620
GCGCGGCCTC CTGGTCTACC CCGAGGTGAA GCGCCTCATG TTCCGAATCG CCATGCGCAT	1680
CCTACTGGGC TGCGAACCCC AACTGGCGGG CGACGGGGAC TCCGAGCAGC AGCTTGTGGA	1740
GGCCTTCGAG GAAATGACCC GCAATCTCTT CTCGCTGCCC ATCGACGTGC CCTTCAGCGG	1800
GCTGTACCGG GTAAGGGCGG CAAACGGGCT GCGGACTAGG GCGCGGGGAC CTGGGCGTCT	1860
GCTCACCGCC GCGCGCTCTC TGCGCTCAGG GCATGAAGGC GCGGAACCTC ATTCACGCGC	1920
GCATCGAGCA GAACATTGCG GCCAAGATCT GCGGGCTGCG GGCATCCGAG GCGGGCCAGG	1980
GCTGCAAAGA CGCGCTGCAG CTGTTGATCG AGCACTCGTG GGAGAGGGGA GAGCGGCTGG	2040
ACATGCAGGT GAGTAGCAGC TTCAGACCAG GCACTGCGGA GTTTGGTCCC CTGGCTTTCC	2100
AAGGCGCTGT TCCTGGGGCC CCCAAAGCGC GCGCCTGGGG CCCAGCTTTC TGGAGTGGGC	2160
GGCCGGCTCA GACTACAGCT ATGGAATCCC GAAGGAAGGC TGAGACACCC GGTCAGGAGA	2220
GCTGCGGAAG GGGCTGCGGM GGAAACTGGG AGCATCCCT AGCCTTTAMC AGGTTTCAAA	2280

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GGGAAAGTTG GAATTTGCAA AAATGTTAAT AAAGAACCTT GCGATTTTAA TAAAACTAAG	2340
ACTTTAACTC AGGAGTTTCC GGTAGRGCGG GGTCGTA CTG GCCTTACTGC TCCAGCTGAA	2400
CTAAAGGGAC GTTGCAATTT GTTTAAAGAT ATTGCTTTCC TTGACTTTCT GTCAGCAAAA	2460
CATTTAGCCC TTCTAGTCTT CCCTCCAGAA CTCTCAGTTC GATTCTGAGT AATCCTTCTG	2520
TCAAACCGCA GGCAGACTTG TGAGAATGTG GGTCTCACTC TATTCTTAGG CACTAAAGCA	2580
ATCTTCAACC GAACTCCTCT TTGGAGGACA CGAAACCACG GCCAGTGCAG CCACATCTCT	2640
GATCACTTAC CTGGGGCTCT ACCCACATGT TCTCCAG	2677

(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

GATCCAGGTT GCTGAAACAT ATCTCCATAT AGGGCAGAAC AATTATCAAA AGCATAAGAA	60
TTGCAGCCAC AGCATAGGGA AGAAAGAGGA GTTTTAAAC CACAACAAA GGGAGAAAGA	120
AGAGAATTTT AACTTACATT TAATTCAAAA GTCTTCAGAG CAACCCGAAA CCCTCCTGGA	180
ACTGGGGGAT TCAGTCGAAG GGTCTCCTTA ATAACACACC CGATGTATYT AAGTTGTTCC	240
AAAATTTCCA TGTCCAACCT GTTGTCTTGA TTGCTCTTGC AAAGTAAACC CTAYCAAAAY	300
AGTCATACAG AGGTGAACAG TYATTTTGTG CTCCAATTAA AATCAGCCCA GCAGACGTAA	360
ACAGGGCTTA AGTGGAGACT AAACCCAAAG GGCCCCATGA TGGGAGAGAC TGGGAGGGGG	420
AAACAGCAGC TAATGGCCAT TTGCCTGCCC AAATCCACTA TCTATTTACA ATCCCAGGAG	480
AATGCTGCTC ACCAGTTAGA AGGACCAAGT TTCTCCCCAC GCCCCCCCAC CCCACACTCA	540
CCACCACCAC CCACACTAAT CAGCTATTCA CACTATGTAT GCCCTTGGAC ACACCAATTC	600
AAGAAAAGTG GAACCTATCT GAGAATCTCC ACGGTTCA CA AAAAGGTGGA GGAGGGGTAG	660
GAATACAAGG TCAAACCCTG CCC	683

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

TCGCGAGGAG CGACCACGGC TTGAAGAGGG GTAGACGAGA CCAGATGCTC CCCGGCGCCC	60
CCTCATGCGG GTTGCGGTCT CTCTCCTCCA CCTCCCTCTC AGCGGAGGAA GTTTCTGCAG	120
ATGAAGCGCA GGAAATACGG CTTTCATCTAC AAGACGCATC TGTTTGGGCG GCCCACGGTG	180
CGGGTGATGG GCGCGGATAA TGTGCGGCGC ATCTTGCTGG GAGAGCACCG GTTGGTGTCG	240
GTGCACTGGC CCGCGTCGGT GCGCACCATC CTGGGCGCTG GCTGCCTCTC CAACCTGCAC	300
GATTCCTCGC ACAAGCAGCG AAAGAAGGTG AGGGTGAGCT GGCAACTCCT TGGCTGGCAG	360
GGAGACCTCA TCCTATGGCT TGGTTCAGGC AAAATAGAAT GCGGGGCGAG GGCTAGTCCT	420
ATGTGGTGGG GACCAGGACC CTCTCTATCT GAGATCCACT TTAGCTTTTC TGCTAGCACG	480
TGGGTTAGTC CTGGGGGGGA CTGAAATTCT TGAAAGGGTA CTCGGAAAGG CGAAGGGGGG	540
GGGGCTGAGG GAAAGTAGAG GATTGTAACA CTCTCTGCTC CTGGGGGGTG CTCAGGTGAT	600
TATGCAGGCC TTCAGCCGCG AGGCACTCCA GTGCTACGTG CCCGTGATCG CTGAGGAAGT	660
CAGCAGTTGT CTGGAGCAGT GGCTAAGCTG CGGCGAGCGC GGCCTCCTGG TCTACCCCGA	720
GGTGAAGCGC CTCATGTTCC GCATCGCCAT GCGCATCCTG CTGGGCTGCG AGCCGGGTCC	780
AGCGGGCGGC GGGGAGGACG AGCAGCAGCT CGTGGAGGCT TTCGAGGAGA TGACCCGCAA	840
TCTCTTCTCT CTTCCCATTG ACGTGCCCTT TAGCGGCCTG TACCGGGTAA GGGCGGTTTG	900
CGGAGTCGGA GTAGGGGAAC GCAAGCTCGG GCATCCGCTC ACCGCCACGC TCTCTCCGCG	960
CTCAGGGCGT GAAGGCGCGG AACCTTATAC ACGCGCGCAT CGAGGAGAAC ATTCGCGCCA	1020
AGATCCGCCG GCTTCAGGCT ACAGAGCCGG ATGGGGGTTG CAAGGACGCG CTGCAGCTCC	1080
TGATTGAGCA CTCGTGGGAG AGGGGAGAGA GGCTGGATAT GCAGGTGAGA AGCAATTTCA	1140
AAAGGTGCCA AGGGCCGGGG AGTGCCTCTG ACTTTCCAGA CACTTTTCT GGGGTCTCCA	1200
AAGCCCTGTC AAGGCCCCAG CTAATTCCAA GTGGGCGGCG ATGCTAGGTC TAGAGCTTTT	1260
CAACCTGTGG GTCGTGACCC CTTACGGAG CCAAACAACC CTTTCAGAAG GGTGCGCTAA	1320
GAGCATCTGC ATATCCGATA TTTACATCAA GAAACATAAC AGTAGCAAAA TTACCGTTAT	1380
GAAGTAGCAA CAAAGATAAT TTTATCGTTG GGGGTCACCA CAACACGAGG AACCGTATTA	1440
AAGGGTGGCA TTGGTCTAGA GAGCTGTGGA AGGGGGTGGC TGAGCAATGG GGAAGATCCC	1500
AAAGTTCAAA GGGCAAGGCT CATCTACAAA GGTTAAAGCG GAAGAGCAGG ATTAAGGGAG	1560
TTTTGCGTTT TTGTTTGTGG TCTTTGACTT TCTATGAACA AAACGGATTT TACCCTTGAA	1620
GTCTTCCGTG CAATATTCTC AGGTCAGGTC TTTGTAACAG TGCTATAAAC TGCACTCAGA	1680

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TCTGTATAAA CTTCCGTTTT TATCCTTAGG CACTAAAACA ATCGTCAACA GAGCTCCTCT	1740
TTGGTGGTCA TGAAACTACA GCCAGTGCTG CGACGTCCT GATCACTTAC CTAGGACTCT	1800
ACCCACATGT CCTCCAGAAA GTTCGAGAAG AGATAAAGAG CAAGGTAGGA TGATTCTAGA	1860
GGTTCCCAT TTGCCTAGGA CATTCCTCTA TTAACCACCA CCACCACCCC CACTGTATAT	1920
AAGTTTGCTC GATACACCCA GTACTATGAC AGTGAAGATC TGAGAGCTAG GTGGGACTGT	1980
GGGGGAGAGA CTCCACCTCG TGAATTTAAA AAGGCAGTTG TTTGTACTGG GCTCTCTCTT	2040
GGGCAGAATT TGACCCTCTC CTCCTCCTCC TCCTCCTCCT CCTCTTCCTC CTCCACCACC	2100
ACCACCATCA CCACCTTTTA TAGAGCAAGG TTCTCCTTTC CCTGACCAAG AACATGAATA	2160
ATGTGATTAG AGCCAATAGC TGATCAGGGT CGCAGTGTTG GTGAGGGCTC AGGGTATGAC	2220
CCTTTATATA CCTGATAAGC AACATTGTCT GGATAATGGG TTTAGGCTGA GGAAGTGTGG	2280
AAAGGAAGGC CATCAGGCCA TCAGCTCTTT CCCTTTTATC CTCTCCCATC CAGACGCCTT	2340
CAGGTTTAGT TAACAGGTGA GTCCTGCTGG GCTGACTTTT TTTTGGAGT GCCCAGGGAT	2400
CCATCACTCA CTTTTTTATC TGTTTCCATA GGGCTTACTT TGCAAGAGCA ATCAAGACAA	2460
CAAGTTAGAC ATGGAAACTT TGGCACAGCT TAAATACACT GGGTGTGTCA TTAAGGAGAC	2520
CCTGCGATTG AATCCTCCGG TTCCAGGAGG GTTTCGGGTT GCTCTGAAGA CTTTGTAGCT	2580
GAATGTGAGT GCACCTCCTG TCCCCACCC CCAGCCCTCG TCCACGTCCA CTCTGCTATG	2640
CTGTTGAGCA TCAGCTGCCC AGAGCAGTGG CTCACTGCCC TTGACAGTGT CCTGCCCTCCT	2700
ATGGTACTGG GAACCAATTT GCTCTCCTCT CTTAATGCCA TCCATGCTAG TAATGACTTT	2760
TTGTTGTTGC AAGCTCAGGG CCGGGATTGT CAATTCCTAG GATTTTTTTT TTTTTTTAAA	2820
CAGGGATACC AGATCCCCAA GGGCTGGAAT GTTATTTACA GTATCTGTGA CACCCACGAT	2880
GTGGCAGATA TCTTCACTAA CAAGGAGGAA TTTAATCCCG ACCGCTTTAT AGTGCCTCAT	2940
CCAGAGGATG CTTCCCGGTT CAGCTTCATT CCATTTGGAG GAGGCCTTCG GAGCTGTGTA	3000
GGCAAAGAGT TTGCAAAAAT TCTTCTTAAG ATATTTACAG TGGAGCTGGC TAGGCACTGT	3060
GATTGGCAGC TTCTAAATGG ACCTCCTACA ATGAAGACAA GCCCCTGTGT GTACCCTGTG	3120
GACAATCTCC CTGCAAGATT TACCCACTTC CAGGGAGATA TCTGATAGCT ATTTCAATTC	3180
TTGGACTTAT TTGAAGTGTA TATTGTTTTT TTTAAAATAG TGTCATGTTG ACTTTATTTA	3240
ATTTCTAAAT GTATAGTATG ATATTTATGT GTCTCTACTA CAGTCCCGTG GTCTTAAATA	3300
TTAAAATAAT GAATTTGTAT GATTTCCCAA TAAAGTAAAA TTAAAAGTG CTTCTCTTGC	3360

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TTTTTAAGAT TCTTGTTGGC AAGCTGCCCCA TGGTGGTACA TTGCTGTAAT ACTAGGACTT      3420
GGAAGGTGGA GGCAAGAAGA GCAGGCATTC AAGGCTAGCC TGGGCTACAG AAATCCTGTC      3480
TTAAACAAAC ACTACAACAA AAAGTCCTGT TAGGGAATCT GACTGGCTCA GTGTTTGTAC      3540
TTTGTGTATT TAAAATGATT TAGAGTGAAA CCATAGGTCT CTCCCCCATG TCAGAAAATA      3600
TATATTATTA TGTGTATGCT GATCCAAAGT ATCTTTGTAA CTTTTTCTAA GGTCATTGAG      3660
ACTTCATATT TTGAAATTGT ATGGAGGCTA GTTATATTAC ATTATTTATT TATTTATTTA      3720
TTTACATTTT TATGGTGCTG GGGATTGGAT CGAAGGCTTC ACACCTCTAG GGCAAGCCCT      3780
TTGTCATTAA GGCGCTGCCT CTCCCTTTCA GCCCAACGTT AATTCTAGAT TCTTTTTTCTT      3840
TGGTGCTTTT GGGAGGTAAA CCTGGGATGC TGCAGTTATT TGGTGGTGGT CGTTGGTTTT      3900
ACTCTAGAGA GAAGGCAACT TTGGGAAGGC AACACTGCTG CTGGTGAGTC GGGAAGCATC      3960
ATCCCAGAGC AACGGGGTCA GCATAGCTAA CATTTTAAAT CAGCATAATG AATCCCTGTC      4020
ATATGGAGGA GGCAGAACTC CTCTTTGAAG TTGATATTTT AGATAAGACA GAGCCAGCCC      4080
CTCTGGTTAT GGACAGTTCT TACCCAAAAT GAAACAGAGA AGAAAACCAC TGGTGTGTCA      4140
CCTTTCCTTA GAAGTGCTTC AGGA      4164

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(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Each N can represent any nucleotide and there can be 0 to 5 N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

TGAACTNNNN NTGAACT 17

(2) INFORMATION FOR SEQ ID NO:40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

TCTGASSAAG KTAAC 15

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(2) INFORMATION FOR SEQ ID NO:41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

CAATTAAAGA

10

(2) INFORMATION FOR SEQ ID NO:42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

CAATTAAAGA TGAAC TTTGG GTGA ACTAAT T

31

(2) INFORMATION FOR SEQ ID NO:43

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

GTAGCACGGA TGGTG

15